

sequence of the human α -interferon gene

GAATTCGGTCGGCAATATGCAGAAATTAACCGCGGGTGGCTCTGAGCCAGCGCGGGGAGGCAGCGCGCGCGCCAGCACCGGACCGCACCGAGGANGAGCCAGCCCGCCG

CTCGCCCCCTTCGGTCCCCACCCCCATCCCGGGCGCCAGCAGGCTCCCGCGCTGGCGCGCACCTCCCTGTTTCTCTCTGGCTGGCGCTGCTGCTCTCGCACCTCACTGCTC

CGCGGGCGCGTCCGCGCCAGTCCGTCTCCCGCGCGCACCGTCTCCGGCGCGCGCTCCCTAAGGATGCTACTGATTTTTCGCGCCACAGGAGACCGGGCTGAGCGCGCGCGCGCGCG

CTCGGCTCTCTCCGAGCAGCCAGCGCGCTGGGACGGC

	1						10									20		
Met	Arg	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Gly	Cys	Gly	Tyr	Leu	Ala	His	Val	Leu	Ala
ATG	AGG	ACC	TTG	GCT	TGC	CTG	CTC	CTC	GGC	TCC	GGA	TAC	CTC	GCC	CAT	GTT	CTC	GCC

30. Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg Leu Ala Arg Ser Cln Ile His Ser Ile Arg Asp Leu Cln Arg Glu Leu Glu Ile
 GAG GAA GCC GAG ATC CCC CGC GAG GTG ATC GAG AGG CTC GCC CGC AGT CAG ATC CAC AGC ATC CGG GAC CTC CAG CGA CTC CTC GAG ATA

GAC	TCC	GTA	GGG	ACT	GAC	GAT	TCT	TTG	GAC	ACC	AGC	CTG	AGA	GCT	CAC	GGG	GTC	CAT	CCC	ACT	AAG	CAT	GTC	CCC	GAG	AAG	OGG	CCC	CTC	Leu	
Asp	Ser	Val	Gly	Ser	Glu	Asp	Ser	Leu	Asp	Thr	Ser	Leu	Arg	Ala	His	Gly	Val	His	Ala	Thr	Lys	His	Val	Pro	Glu	Pro	Glu	Lys	Arg	Pro	Leu

CCC ATT	CGG	ACG	AAC	AGA	ACC	ATC	GAG	GAA	GCT	GTC	CCC	GCT	GTC	TGC	AAG	ACC	ACG	ACG	GTC	Val	Ile	Tyr	Glu	Ile	Pro	Arg	Ser	Gln	Val
Pro	Ile	Arg	Arg	Lys	Arg	Ser	Ile	Glu	Glu	Ala	Val	Pro	Ala	Val	Cys	Lys	Thr	Arg	Thr	Val	Ile	Tyr	Glu	Ile	Pro	Arg	Ser	Gln	Val

Asp Pro Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys

120 130 140

GAC CCC ACG TCC GCC AAC TTC CTC ATC TCG CCC CCG TGG GAG GTG AAA CGC TGC ACC GGC GGC GGC ACC AGC AGC AGC AGC
Gln Pro Ser Arg Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr;Val Arg Lys Pro Lys Leu Lys Glu Val Gln Val Arg
CAG CCC TCC CGC GTC CAC CAC CAC CGC AGC GTC ANG GTC GCC ANG GTC GAA TAC GTC AGG AAG CCA AAA TTA AAA GAA GTC CAG GTG AGC

150. 160 170

[illegible]

	210	211	
Lys Lys Arg Lys Arg Lys Arg Leu Lys Pro Thr	OC		
AAA AAA CCG AAA AGA AAA AGC TTA AAA CCC ACC TAA			AGCAGCCACCAGATGTCAGCTAGGATGAGCCGAGCCCTTCTCTGCACATGATGTACATGCGGTGTA

CAATTCCTGAACCTACTACTATCGGTCGCTTTATTGCCAGTGTCCGCTCTTTGTTCTCCTCCCTGAAAAAAGTGTCTCGAGAACACTCGGAGAACAGACAGTCGCACATTGTTTAAAT

GTGACATCAAGCAAGTATTGTAGCCACTGCGTAGCAGTAAGANGCTTCCTTGTCAAAAGAGAGAGAGAGAAAGCAAAAAGGGAATTC

Translated Mol. Weight = 24046.60

Figure 1

GAATTCGGTCCGCAATATGCAGAAATTACCGGGCCGGCTCGCTCTGTAAGCCAGCGGGAGGAGCGGGCCGCGCCAGCACCGGCAACGCCAGCGAGGAGCCAGCCCGCCGCGC

CTCGCGCCCTTCGGTCCCGCCATCCCGCGGGCCAGGAGGCTCCCGCGGCTGGCGGCACCTCCCTGTTTCTCCTCTCTGGCTGGCGCTGCTGCTCTCGGCACCTCACTGCTGCTC

CGCGGGCGCGCTCGCGCCAGCTCCGTCTCCCGCGCGCCACCCCTCTCTCGGGCCGCGCTCCCTAAGGATGGTACTGATTTTCCCGCCACAGGAGACCGGCTGGAGCCCGCGCCCGCGCGC

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala His Val Leu Ala
 ATG AGG ACC TTG GCT TGC CTG CTG CTC CTC GGC TGC GGA TAC CTC GCC CAT GTT CTG GCC

30 40 50
 Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu Glu Ile
 GAG GAA GCC GAG ATC CCC CGC GAG CTC ATC GAG AGG CTG GCC CGC AGT CAG ATC CAC AGC ATC CGG GAC CTC CAG CGA CTC CTC GAG ATA

60 70 80
 Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 GAC TCC GTA CGG AGT GAG GAT TCT TTG GAC ACC AGC CTG AGA GCT CAC GGG GTC CAT GCC ACT AAG CAT CTG CCC GAG AAG CGG CCC CTG

90 100 110
 Pr Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val
 CCC ATT CGG ACG AAG AGA AGC ATC GAG GAA GCT GTC CCC GCT GTC TGC ANG ACC AGG ACG GTC ATT TAC GAG ATT CCT CGG ACT CAG GTC

120 130 140
 Asp Pro Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys
 GAC CCC ACG TCC GCC AAC TTC CTG ATC TGG CCC CGC TGC GTC GAG CTG AAA CGC TGC ACC GGC TGC TGC AAC ACG AGC AGT GTC AAG TGC

150 160 170
 Gln Pro Ser Arg Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys Lys Pro Lys Leu Lys Glu Val Gln Val Arg
 CAG CCC TCC CGC GTC CAC CAC CGC ACG GTC AAG GTG GCC AAG GTG GAA TAC GTC AGG AAG AAG CCA AAA TTA AAA GAA GTC CAG GTG ACG

180 190 196
 Leu Glu Glu His Leu Glu Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp Thr Asp Val Arg
 TTA GAG GAG CAT TTG GAG TGC GCC TGC GCG ACC ACA ACG CTG AAT CCG GAT TAT CGG GAA GAG GAC ACG GAT GTG AGG TGA GGATGACCGGCA

GGCCCTTCTCGGCACATGATGTACATGGCGGTGTACATTCCTGGAACCTACTATGTACGGTGGCTTTATTGCCAGTGTGCGGTCTTTCTCTCCGTGAAAACCTGTCTCGAGAACAC

TCCGAGACAACAAAGACAGTGCACATTTGTTTAAATGTGACATCAACCAAGTATTGTAGCACCTCGGTGAGCAGTANGAAGCTTCTGTCAAAGACAGACAGACAAAGAAAAA

AAGGAATTC

AACGAATTC

Translated Mol. Weight = 22256.17

Figure 2.

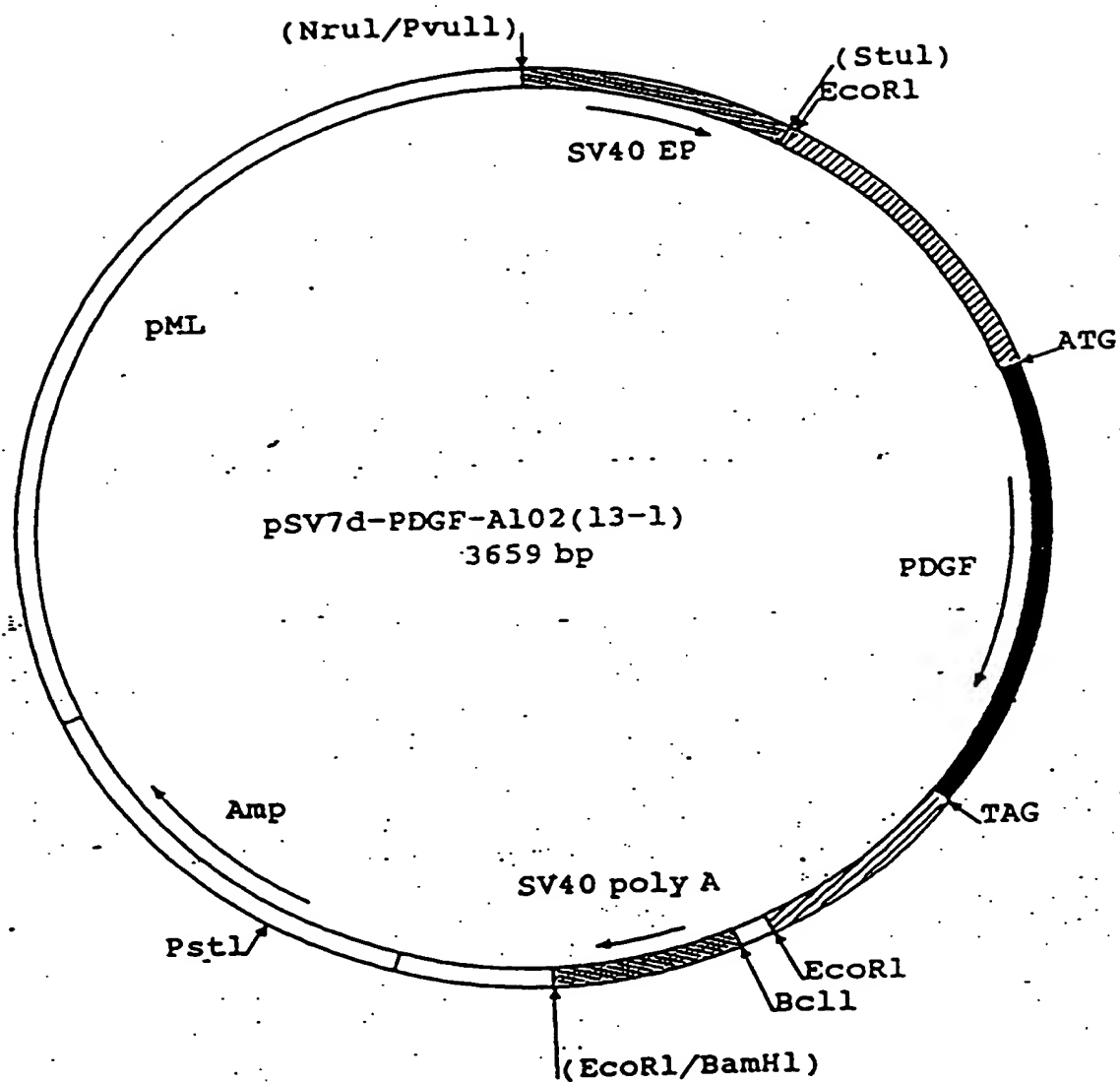
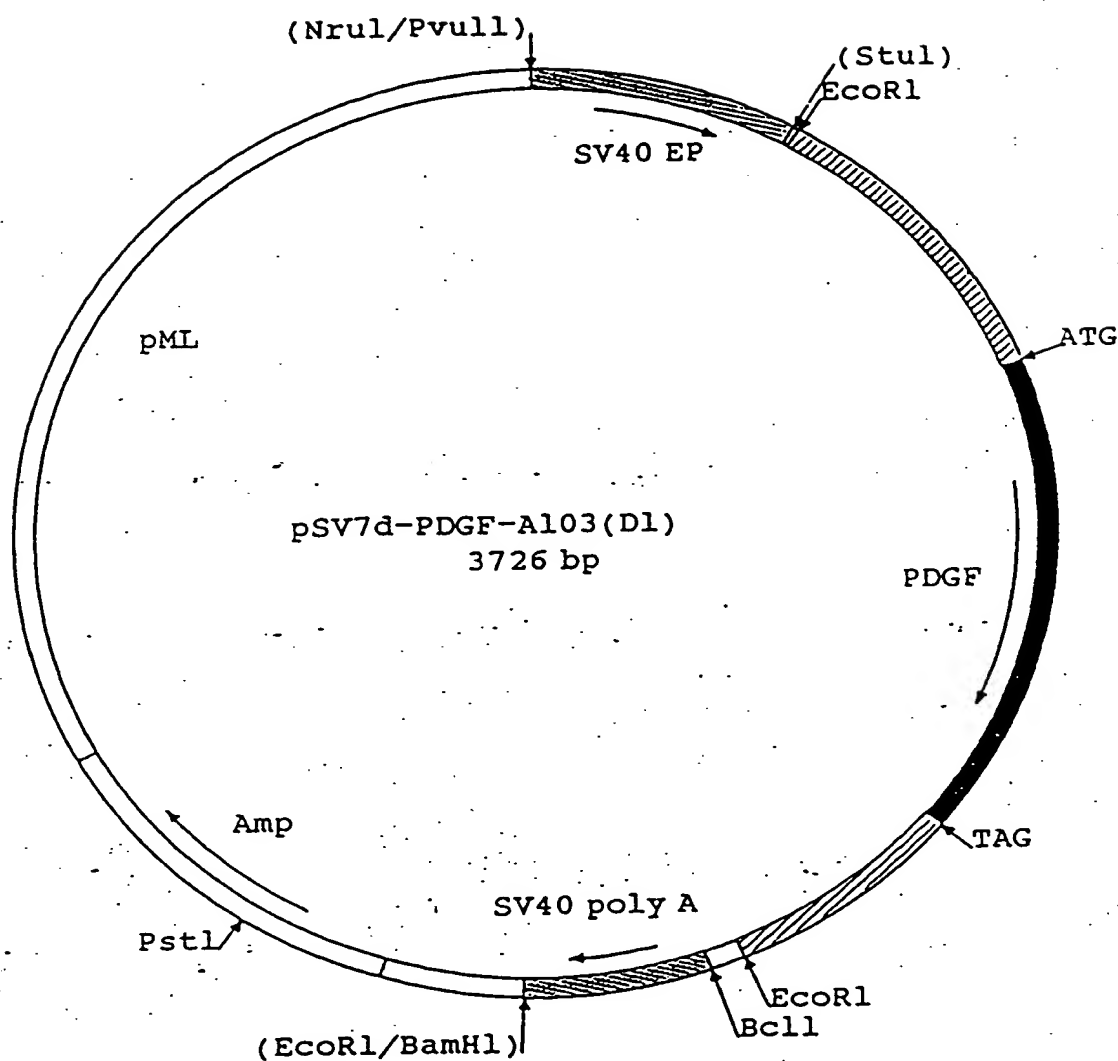
Figure 3.

Figure 4.



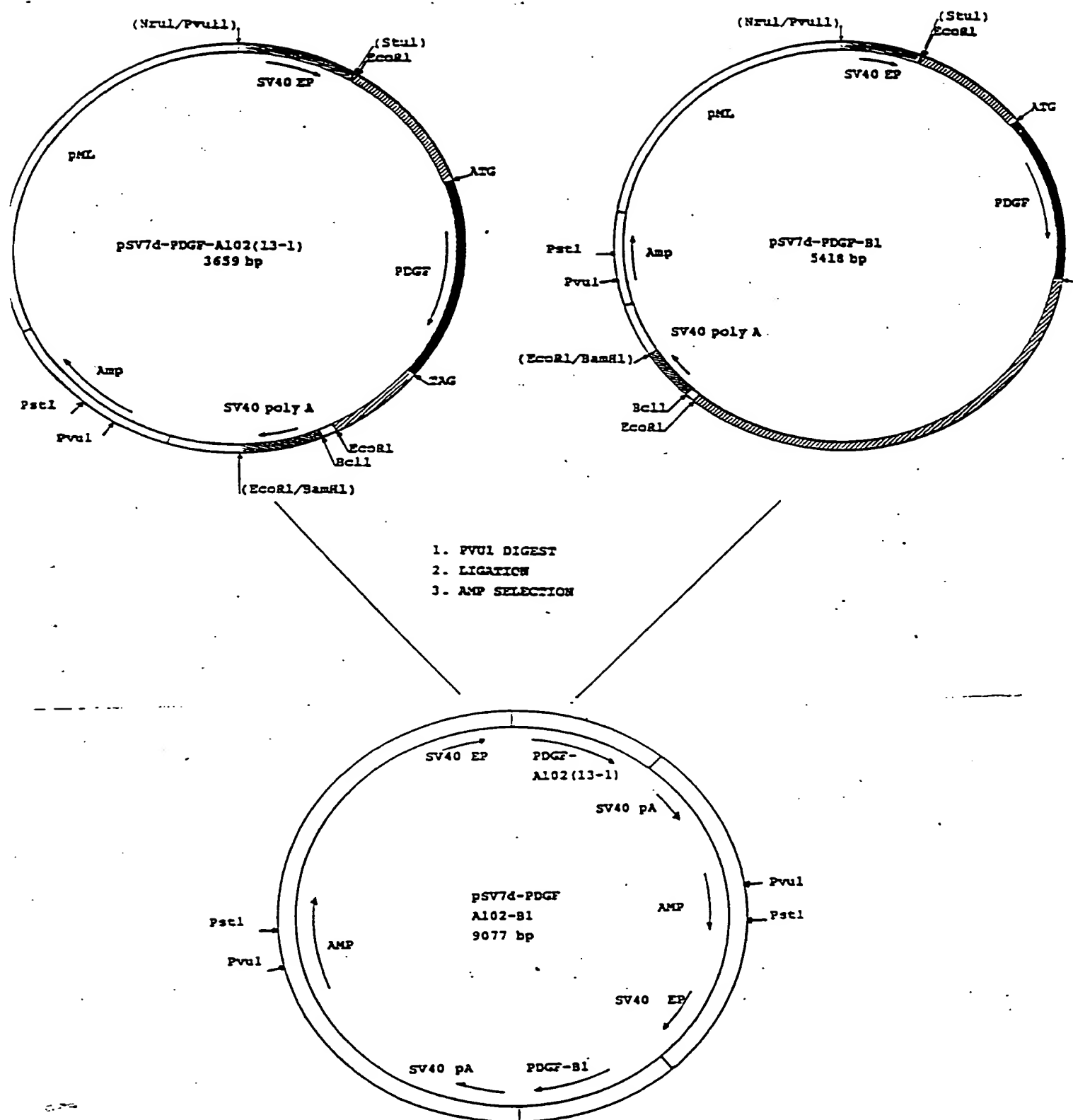


Figure 5

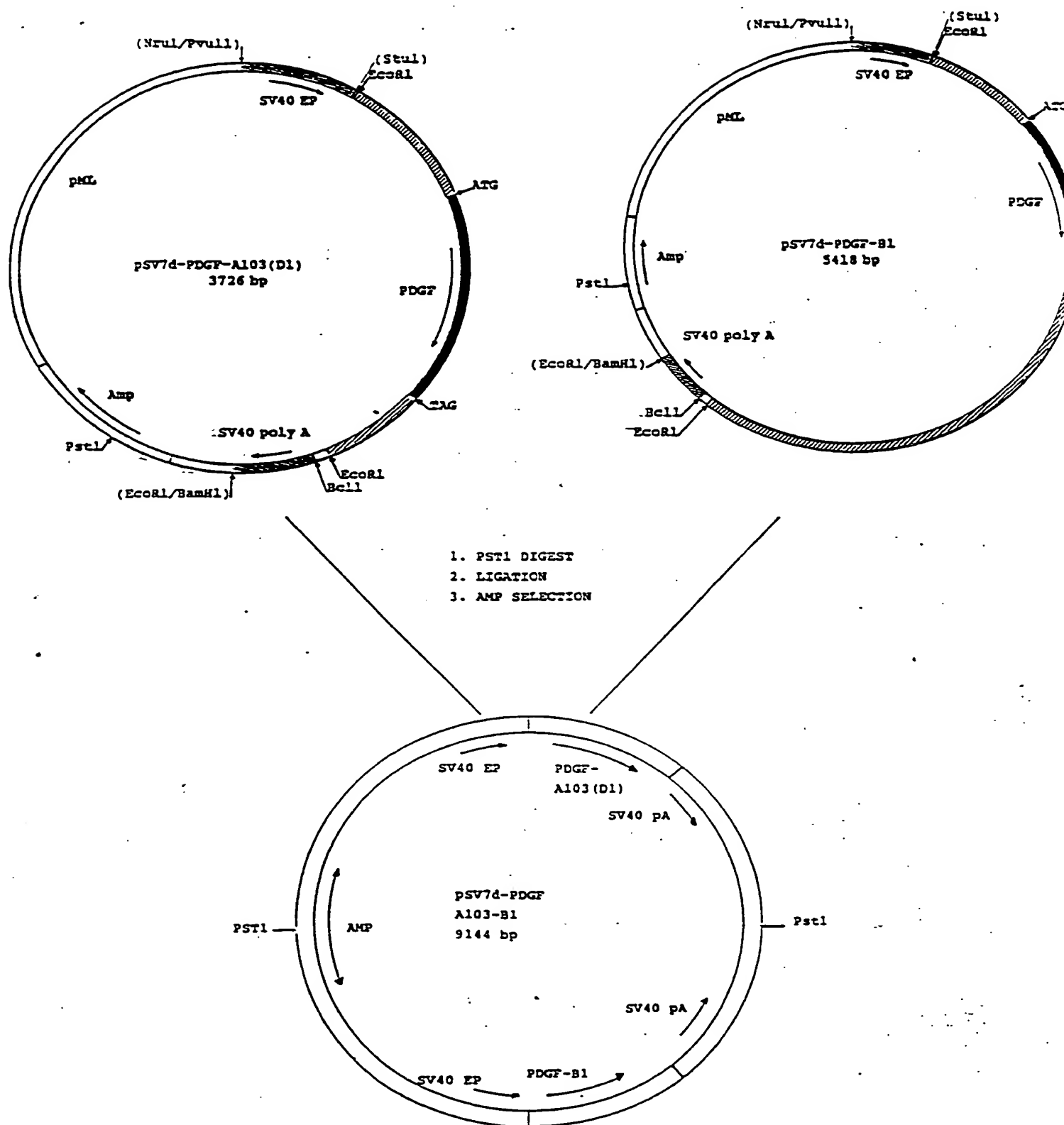


Figure 6

Sequence of SV: early promoter, polylinker, and SV40
poly A addition region from pSV7d

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| 1/2 PVuII site SV40 early promoter --->
CTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGT
GACACCTTACACACAGTCAATCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCA

61  ATGCAAAGCATGCATCTCAATTAGTCAGCAAGGAAAGTCCCCAGGCTCCCCAGCAGGCAG
    TACGTTTCGTACGTAGAGTTAATCAGTCGTTCTTTCAGGGGTCCGAGGGGTCGTCCGTC

68  SPH1

121  AAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCC
    TTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGG

132  SPH1

181  CATCCCGCCCCTAACTCCGCCCAGTTCGCCCATTTCTCCGCCCCATGGCTGACTAATTTT
    GTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAA

223  NCOI,

241  TTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAAG
    AAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTTC

263  BGL1

      | -polylinker-->                                OC  OP  OP
301  AGGCTTTTTTGGAGGAGATCGAATTCGCGGTCTAGAGGATCCGTCGACCTAGATAAGTA
    TCCGAAAAAACCTCCTCTAGCTTAAGGGCCCAGATCTCCTAGGCAGCTGGATCTATTCAT

321  ECOR1, 326  SmaI  XmaI, 332  XbaI, 338  BamHI, 344  SalI,

361  ATGATCATAATCAGCCATATCACATCTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCA
    TACTAGTATTAGTCGGTATAGTGTAGACATCTCCAAAATGAACGAAATTTTTTGGAGGGT

362  BclI, 405  DraI,

421  CACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATT
    GTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAA

466  HpaI

481  GCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTCACAAATAAAGCATTT
    CGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAA

541  TTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCCGCTCATGAGACAATAACCTT
    AAAAGTGACGTAAGATCAACACCAACAGGTTTGAGTAGGCGAGTACTCTGTTATTGGGA

      End of SV40---->||-pBR322 (pos. 4210)->

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Figure 7

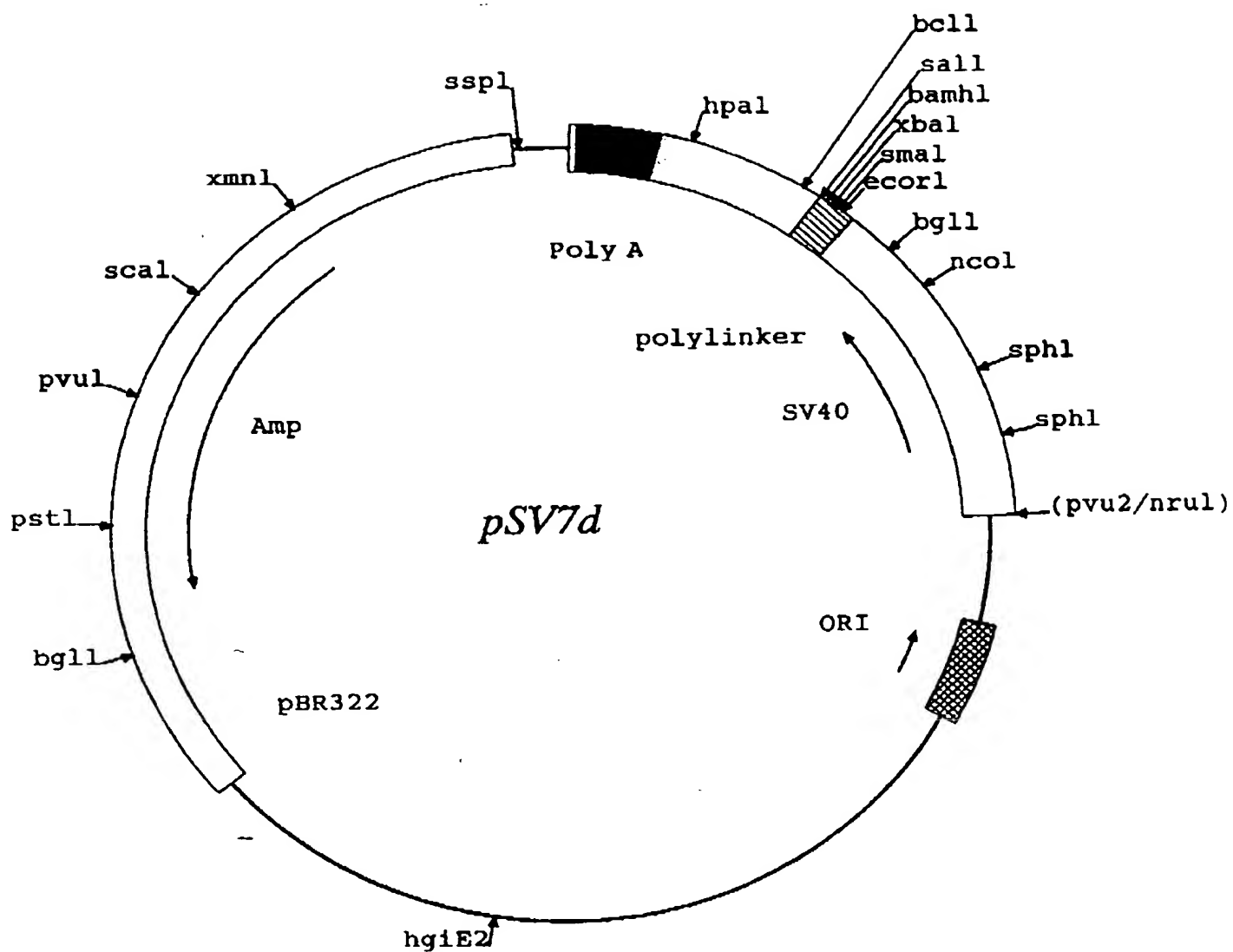


Figure 8

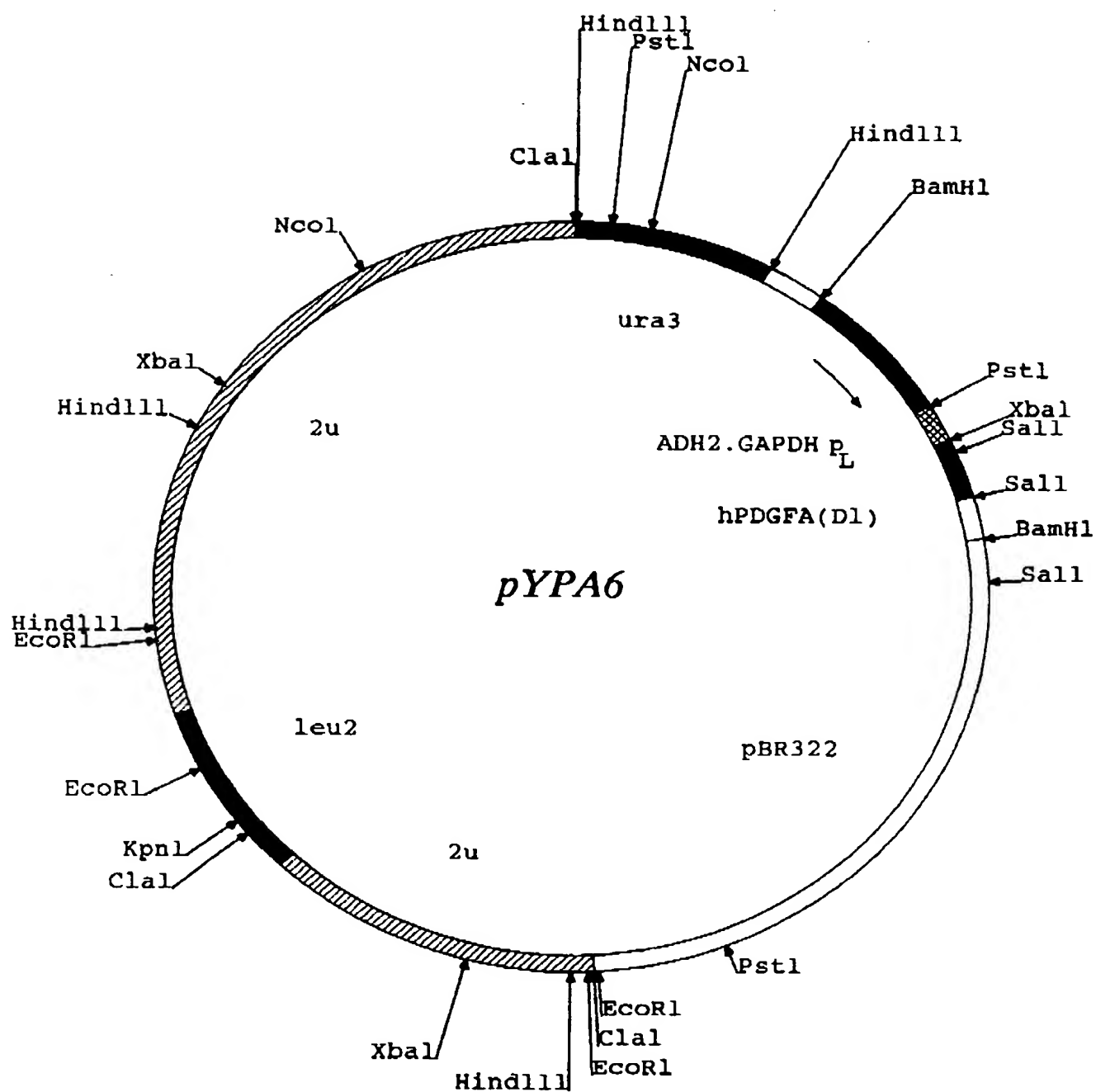


Figure 9

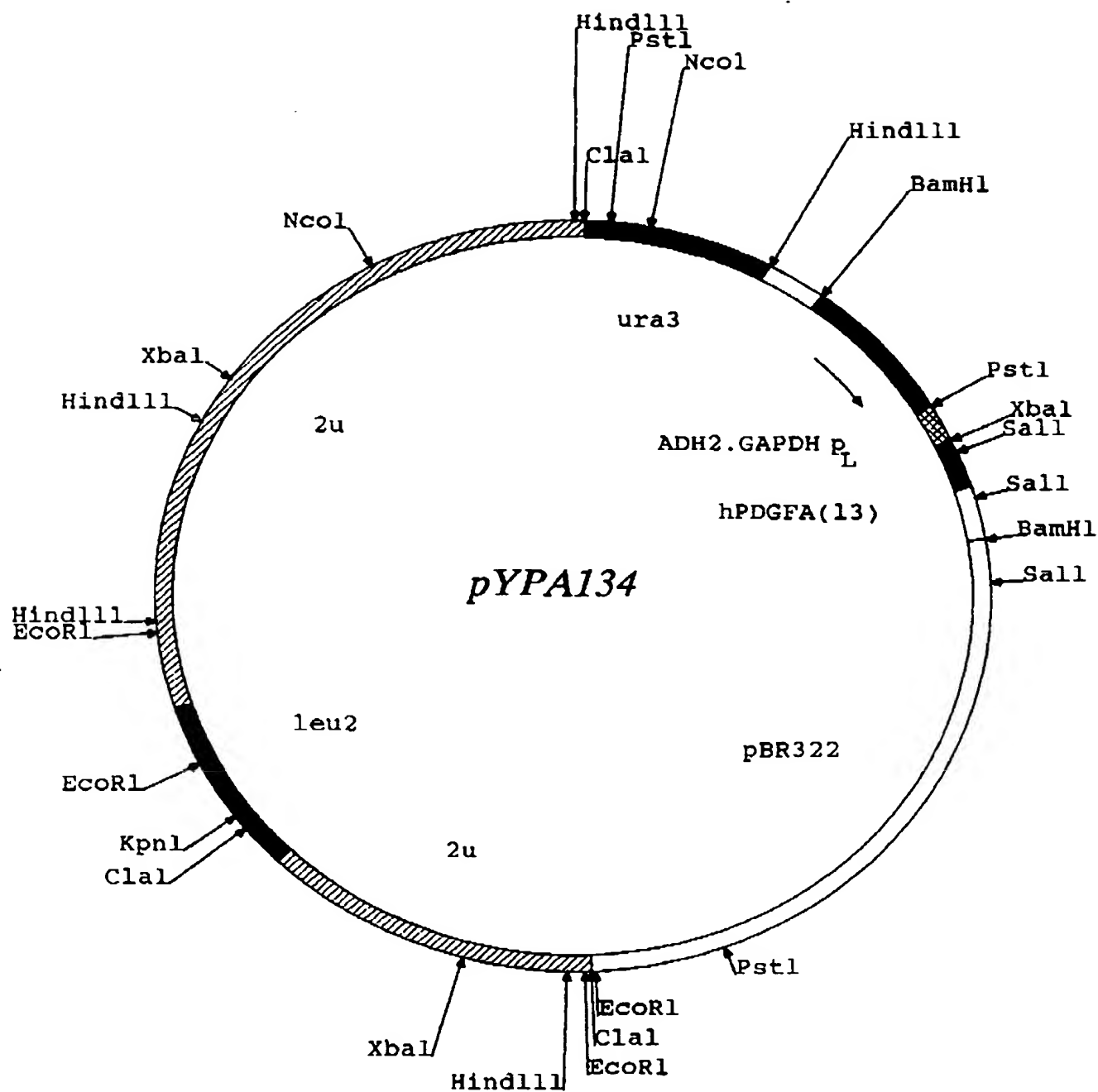


Figure 10

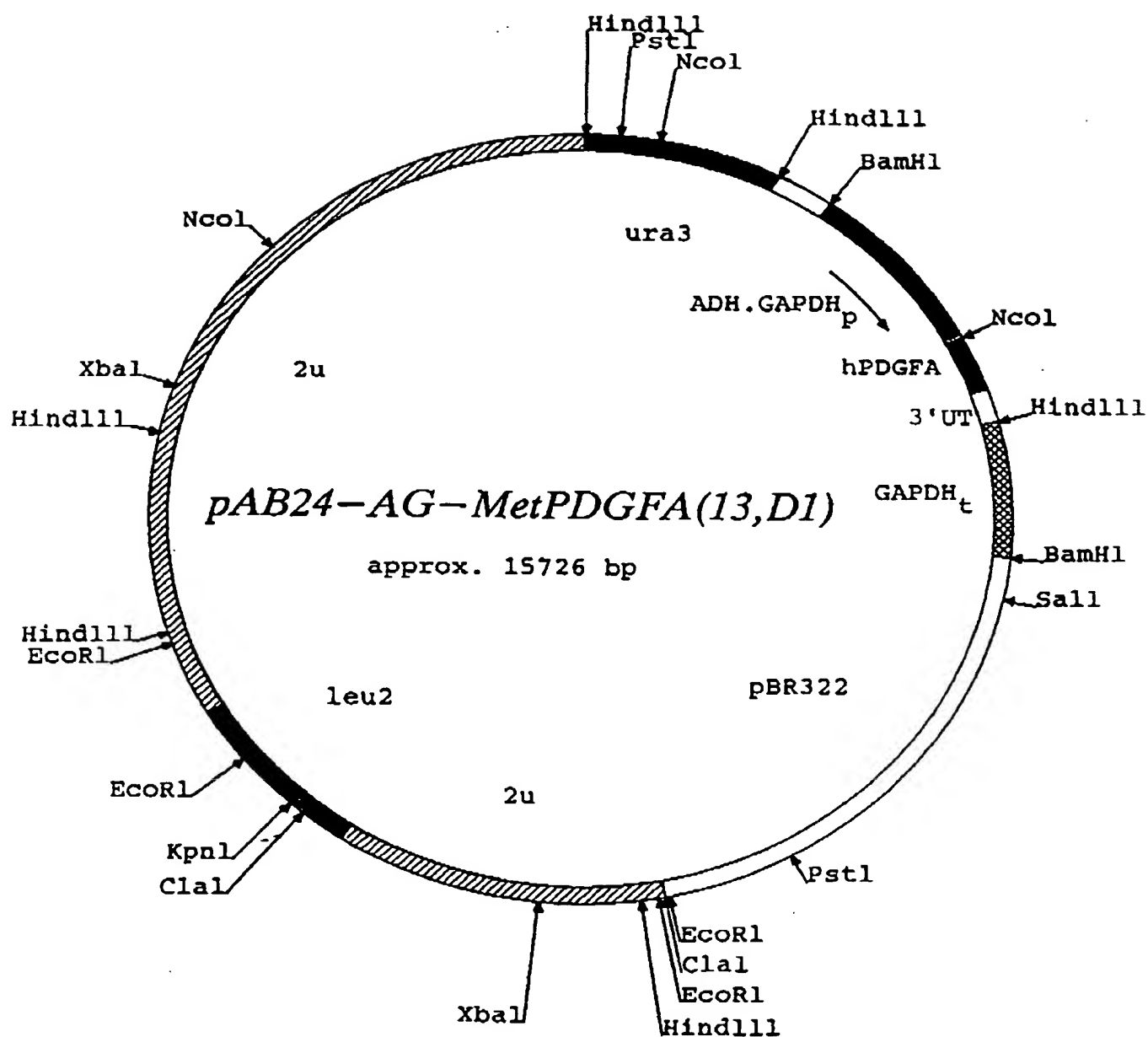


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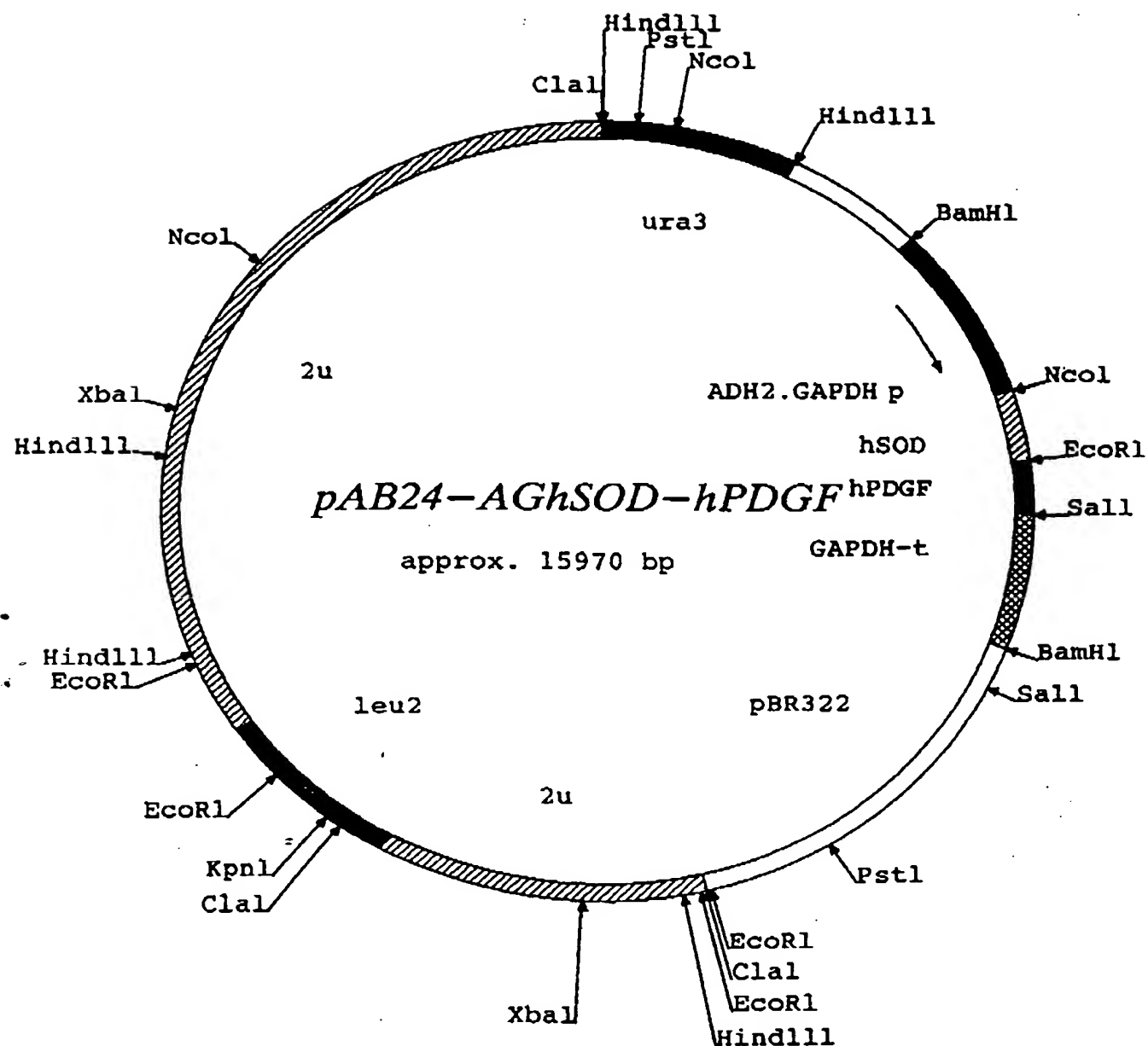


Figure 12

Figure 13.

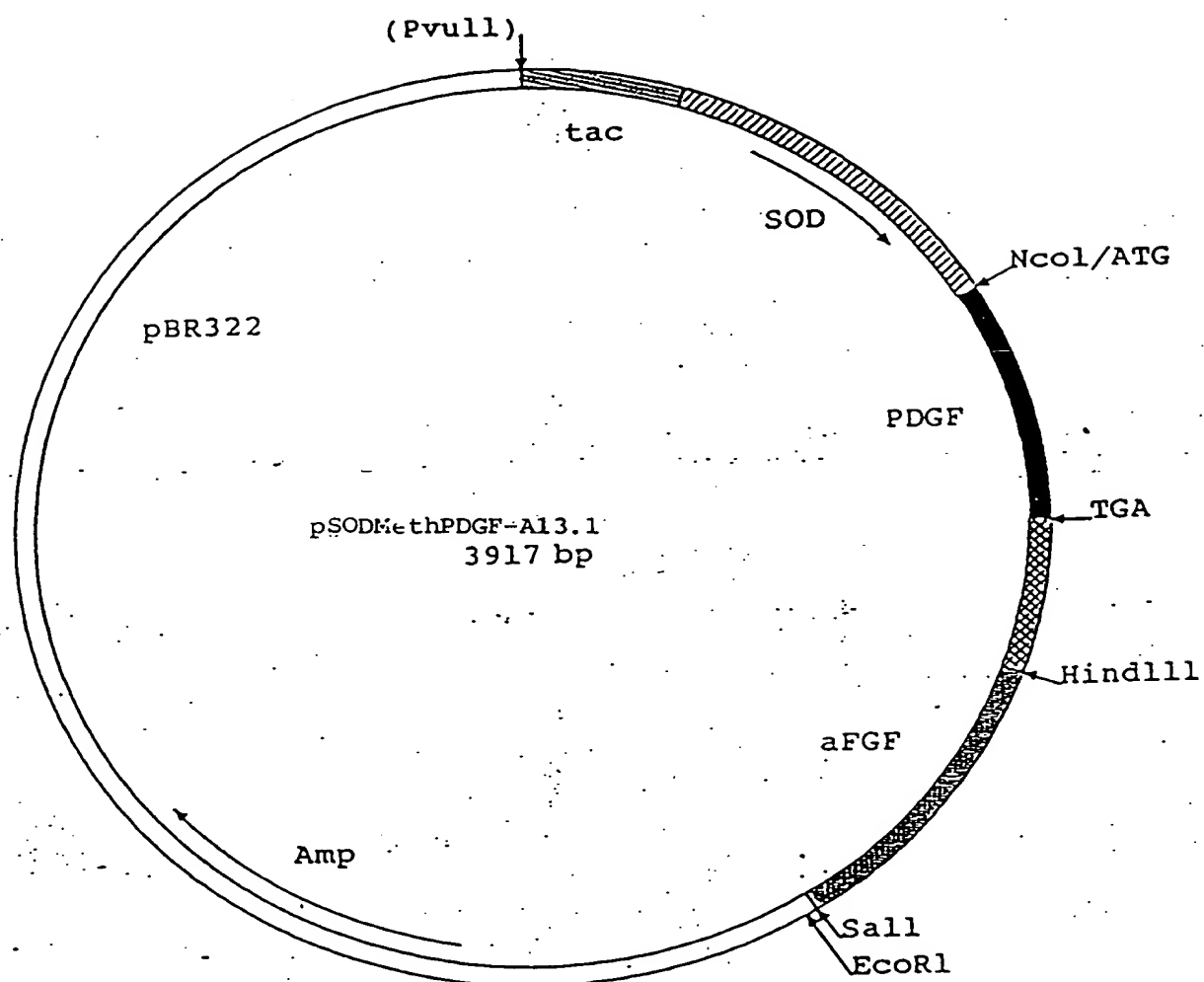


Figure 14

